

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/567,808

Source:

JF420

Date Processed by STIC:

02/16/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/567,808

DATE: 02/16/2006
TIME: 12:55:34

Input Set : A:\08321-0136PC.TXT
Output Set: N:\CRF4\02162006\J567808.raw

4 <110> APPLICANT: Thomas Jefferson University
5 Albert J. Wong
7 <120> TITLE OF INVENTION: METHOD FOR RAPID IDENTIFICATION OF
8 ALTERNATIVE SPLICING
10 <130> FILE REFERENCE: 08321-0136PC
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/567,808
C--> 12 <141> CURRENT FILING DATE: 2006-02-08
12 <150> PRIOR APPLICATION NUMBER: 60/493,759
13 <151> PRIOR FILING DATE: 2003-08-08
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 22
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: (selectable tag)
27 <400> SEQUENCE: 1
28 gtcatgcata gcaattgteg aov
30 <210> SEQ ID NO: 2
31 <211> LENGTH: 17
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: (selectable tag)
38 <400> SEQUENCE: 2
39 tcccecgagg ggaatcg
41 <210> SEQ ID NO: 3
42 <211> LENGTH: 27
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: (selectable tag)
49 <400> SEQUENCE: 3
50 atgcatagca acctcacgtg-tgaateg
52 <210> SEQ ID NO: 4
53 <211> LENGTH: 21
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: affinity medium
60 <400> SEQUENCE: 4
61 acacgtgagg ttgctatgca t

Does Not Comply
Corrected Diskette Needed
CPR-1,2)

Invalid Response.
What is the Source of
genetic material?
Pls see Item # 11
on Error Summary
sheet

17

27

21

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/567,808

DATE: 02/16/2006
TIME: 12:55:34

Input Set : A:\08321-0136PC.TXT
Output Set: N:\CRF4\02162006\J567808.raw

63 <210> SEQ ID NO: 5
64 <211> LENGTH: 58
65 <212> TYPE: DNA
66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: polynucleotide linking moiety
71 <400> SEQUENCE: 5
72 acacgatccg cagatgtccg cagttattcc ttttttggaa taactgcgga catctgcg 58
74 <210> SEQ ID NO: 6
75 <211> LENGTH: 30
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: arbitrary sequence
82 <400> SEQUENCE: 6
83 aaattcctat gcagtctcaa tggactgtgt

? Same error

? Same error

30

VERIFICATION SUMMARY

DATE: 02/16/2006

PATENT APPLICATION: US/10/567,808

TIME: 12:55:35

Input Set : A:\08321-0136PC.TXT

Output Set: N:\CRF4\02162006\J567808.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/567,808

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
 The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
 The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
 The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
 The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
 Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
 Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
 Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES)
 Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
 Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
 Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa
 "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid